AMENDMENTS TO THE CLAIMS

1. **(Currently amended)** A computer-based method for identifying conserved peptide motifs useful as drug targets for use in a host organism, wherein said method comprises the steps of:

i) computationally generating using one or more computer processors overlapping peptide sequences of length 'N' from selected pathogenic organisms using a peptide library creating software program (PEPLIB),

ii) computationally sorting the peptide sequences of length 'N' according to amino acid sequence,

iii) computationally matching using one or more computer processors the sorted peptide sequences of length 'N' of the selected pathogenic organisms to produce exactly matched common peptide sequences using a peptide library matching software program (PEMLIMP),

iv) computationally locating the matched common peptide sequences in their corresponding protein sequences to provide locations of said matched common peptide sequences and subsequently labeling the matched common peptide sequences with their origin and location using a peptide extraction software program (PEPEXTRACT);

v) computationally joining overlapping common peptide sequences to obtain extended conserved peptide sequences using a peptide stitching software program (PEPSTITCH);

vi) comparing said extended conserved peptide sequences obtained in step (v) to host organism protein sequences to identify conserved peptide sequences from said selected pathogenic organisms which are not present in host proteins; and

vii) communicating said conserved peptide sequences from said selected pathogenic organisms not present in said host proteins to a user to obtain conserved peptide motifs useful as drug targets for use in a host organism, wherein all of said steps are performed on ~~said~~ a computer.

2. **(Previously presented)** The method of claim 1, wherein 'N' is at least 4.

3. **(Previously presented)** The method of claim 1 wherein the selected pathogenic organisms include at least one of: Mycoplasma pneumoniae, Helicobacter pylori, Hemophilus influenzae, Mycobacterium tuberculosis, Mycoplasma genitalium, Bacillus subtilis, and Escherichia coli.

4. **(Previously presented)** The method of claim 1, wherein the extended conserved peptide sequences comprise one or more of the following sequences:

1. AAQSIGEPGTQLT (SEQ ID NO:1)
2. AGDGTTTAT (SEQ ID NO:2)
3. AGRHGNKG (SEQ ID NO:3)
4. AHIDAGKTTT (SEQ ID NO:4)
5. CPIETPEG (SEQ ID NO:5)
6. DEPSIGLH (SEQ ID NO:6)
7. DEPTSALD (SEQ ID NO:7)
8. DEPTTALDVT (SEQ ID NO:8)
9. DHAGIATQ (SEQ ID NO:9)
10. DHPHGGGEG (SEQ ID NO:10)
11. DLGGGTFD (SEQ ID NO:11)
12. DVLDTWFSS (SEQ ID NO:12)
13. ERERGITI (SEQ ID NO:13)
14. ERGITITSAAT (SEQ ID NO:14)
15. ESRRIDNQLRGR (SEQ ID NO:15)
16. FSGGQRQR (SEQ ID NO:16)
17. GEPGVGKTA (SEQ ID NO:17)
18. GFDYLRDN (SEQ ID NO:18)
19. GHNLQEHS (SEQ ID NO:19)
20. GIDLGTTNS (SEQ ID NO:20)
21. GINLLREGLD (SEQ ID NO:21)
22. GIVGLPNVGKS (SEQ ID NO:22)
23. GKSSLLNA (SEQ ID NO:23)
24. GLTGRKIIVDTYG (SEQ ID NO:24)
25. GPPGTGKTLLA (SEQ ID NO:25)
26. GPPGVGKT (SEQ ID NO:26)
27. GSGKTTLL (SEQ ID NO:27)
28. GTRIFGPV (SEQ ID NO: 28)
35. KMSKSKGN (SEQ ID NO: 35)
36. KMSKSLGN (SEQ ID NO:36)
37. KNMITGAAQMDGAIL (SEQ ID NO:37)
38. KPNSALRK (SEQ ID NO:38)
39. LFGGAGVGKTV (SEQ ID NO:39)
40. LGPSGCGK (SEQ ID NO:40)
41. LHAGGKFD (SEQ ID NO:41)
42. LIDEARTPLIISG (SEQ ID NO:42)
43. LLNRAPTLH (SEQ ID NO:43)
44. LPDKAIDLIDE (SEQ ID NO:44)
45. LPGKLADC (SEQ ID NO:45)
46. LSGGQQQR (SEQ ID NO:46)
47. MGHVDHGKT (SEQ ID NO:47)
48. NADFDGDQMAVH (SEQ ID NO:48)
49. NGAGKSTL (SEQ ID NO:49)
50. NLLGKRVD (SEQ ID NO:50)
51. NTDAEGRL (SEQ ID NO:51)
52. PSAVGYQPTLA (SEQ ID NO:52)
53. QRVALARA (SEQ ID NO:53)
54. QRYKGLGEM (SEQ ID NO:54)
55. RDGLKPVHRR (SEQ ID NO:55)
56. SALDVSIQA (SEQ ID NO:56)
57. SGGLHGVG (SEQ ID NO:57)
58. SGSGKSSL (SEQ ID NO:58)
59. SGSGKSTL (SEQ ID NO:59)
60. SVFAGVGERTREGND (SEQ ID NO:60)
61. TGRTHQIRVH (SEQ ID NO:61)
62. TGVSGSGKS (SEQ ID NO:62)

29. IDTPGHVDFT (SEQ ID NO:29)
30. ILAHIDHGKSTL (SEQ ID NO:30)
31. INGFGRIGR (SEQ ID NO:31)
32. IREGGRTVG (SEQ ID NO:32)
33. IVGESGSGKS (SEQ ID NO:33)
34. KFSTYATWWI (SEQ ID NO:34)
63. TLSGGEAQRI (SEQ ID NO: 63)
64. TNKYAEGYP (SEQ ID NO:64)
65. TPRSNPATY (SEQ ID NO:65)
66. VEGDSAGG (SEQ ID NO:66); and
67. VRKRPGMYIG (SEQ ID NO:67)

5. **(Canceled)**

6. **(Previously presented)** The method of any one of claims 1-4 wherein the conserved peptide sequences are found within the sequences of at least one of the following proteins:

I DNA DIRECTED RNA POLYMERASE BETA CHAIN
II EXONUCLEASE ABC SUBUNIT A
III EXONUCLEASE ABC SUBUNIT B
IV DNA GYRASE SUBUNIT B
V ATP SYNTHASE BETA CHAIN
VI S-ADENOSYLMETHIONINE SYNTHETASE
VII GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE
VIII ELONGATION FACTOR G (EF-G)
IX ELONGATION FACTOR TU (EF-TU)
X 30S RIBOSOMAL PROTEIN S12
XI 50S RIBOSOMAL PROTEIN L12
XII 50S RIBOSOMAL PROTEIN L14
XIII VALYL tRNA SYNTHETASE
XIV CELL DIVISION PROTEIN FtSH HOMOLOG
XV DnaK PROTEIN (HSP70)
XVI GTP BINDING PROTEIN LepA; and
XVII OLIGOPEPTIDE TRANSPORT ATP BINDING PROTEIN OPPF.

7. (**Previously presented**) The method of claim 1, wherein step (iii) comprises:

selecting organism names from a menu;

iteratively comparing peptide sequences of a first organism to sorted peptide sequences of a second organism; and

writing matched sequences to a first file for the first organism and to a second file for the second organism.

8. (**Previously presented**) The method of claim 1 wherein step (iv) comprises:

selecting protein sequences;

iteratively locating matched peptide sequences in the selected protein sequences; and

if the matched peptide is found in one of the selected protein sequences, labeling the matched peptide sequence in a file associated with the selected protein sequence with: a) a protein identification number (PID), b) a location in the protein sequence, and c) a name of a pathogenic organism chosen from the group of selected pathogenic organisms of step iii).

9. (**Previously presented**) The method of claim 1, wherein said overlapping common peptide sequences in step (v) are computationally joined by:

iteratively comparing matched peptide sequences on matched peptide locations;

determining overlapping matched common peptides; and

determining extended conserved peptide sequences based on overlapping matched common peptides.

10-12. (**Canceled**)